

FIG. 1

FIG. 26

~~FIG. 2a~~

CGT GGA CCT TGG GAC GAA GCT GCA GAT CAA ATC GCT GCA GGT TCA 720
Arg Gly Pro Trp Asp Glu Ala Ala Asp Gln Ile Ala Ala Gly Ser [240]

GTG CTT GAA GGT ACT GTT AAG CGT GTG AAG GAC TTT GGT GCC TTT 765
Val Leu Glu Gly Thr Val Lys Arg Val Lys Asp Phe Gly Ala Phe [255]

GTT GAA ATT TTG CCT GGT ATC GAA GGT CTT GTG CAC GTG TCA CAA 810
Val Glu Ile Leu Pro Gly Ile Glu Gly Leu Val His Val Ser Gln [270]

ATT TCA AAC AAG CGT ATT GAA AAC CCA TCA GAA GTT TTG AAG TCT 855
Ile Ser Asn Lys Arg Ile Glu Asn Pro Ser Glu Val Leu Lys Ser [285]

GGT GAC AAG GTA CAA GTG AAG GTA TTG GAC ATT AAG CCA GCC GAA 900
Gly Asp Lys Val Gln Val Lys Val Leu Asp Ile Lys Pro Ala Glu [300]

GAA CGT ATT TCA TTG TCA ATG AAG GCT TTG GAA GAA AAG CCA GAA 945
Glu Arg Ile Ser Leu Ser Met Lys Ala Leu Glu Glu Lys Pro Glu [315]

CGT GAA GAT CGT CGT GGT AAC GAT GGT TCA GCT TCA CGT GCT GAT 990
Arg Glu Asp Arg Arg Gly Asn Asp Gly Ser Ala Ser Arg Ala Asp [330]

ATC GCT GCT TAC AAG CAA CAA GAT GAC TCA GCC GCA ACA TTG GGT 1035
Ile Ala Ala Tyr Lys Gln Gln Asp Asp Ser Ala Ala Thr Leu Gly [345]

GAC ATC TTT GGT GAT AAG TTG TAA GAGGCATCAACATAAAAGAGCTGGTTC 1086
Asp Ile Phe Gly Asp Lys Leu *** [352]

GCCAGTTCTTTTATTTTGAAGAAAAATTGAGTGGGCATTAGTGGGCGCTCACGGTATG 1145

AAAAAGGAGGTGCGATTATGGCAGCACCAGTAGTAGCCATTGTTGGCGACCAAACGTGG 1204

GAAAATCGACTATCTTTAACCGGATGGCCGGAGAACGTATTGCAATTGTTGAAGATCAA 1263

CCAGGGGTAACACGCGATCGTTTGTACGCGCCAGCCGAATGGTTGAATTAT 1314

006645-0304

FIG. 3a
FIG. 3

HS1	63	SFAEGD	TVDAK	INAVR	GGLVD	NGVRG	FVPAS	MVAER	FVSD	LNQF	KNKDI	KAQV	IEI	121
ES1	101	AYEDAE	--TG	VINGK	-K--FT	ELD--I	-A-L	-G-L-	DV-P	-R-TL	HLEG	-ELEFK	--KL	159
RS1	107	K-EA-ER	-EG	IIF-Q	-K--FT	-LD-AVA	-L-R	-Q-DI	-PIR-VTP	ADAQ	PAAL	RNLKM	165	
PS1	1	E--TG	VINGK	-K--FT	EL--I	-A-L	-G-L-	DV-P	-R-TT	HLEG	-ELEFK	--KL	54	
CS1	182	--DW	-KG-IV	G-NK--V	VAL-E	-L-----	F-Q	ISSK	-SAE	ELLE	-E-PL	KFV-V	236	
								a	b	c				
								****	*****	***				
HS1	122	DPANAR	LILSR	KAVAAQ	ERAAQL	AEVFS	KL	SVGE	VEGT	VARLT	D	FGAFV	DLGGVDGLV	180
ES1	160	-QKR	NNVV--R	-IES-NS	-ERD	QLLEN-QE	-ME	-K-I	-KN--Y	-----	-----	-----	-L	218
RS1	166	-KRR	GNIV--RT	-LEES--E	-RS	-IVQN-EE	-Q---V	-KNI--Y	-----	-----	-----	-----	-L	224
PS1	55	-QKR	NNVV--R	-IES-SS	-ERD	QLLEN-QE	-ME	-K-I	-KN--Y	-----	-----	-----	-L	113
CS1	237	-EEQ	S--VM	-NRKAM	-DSQ-M	-DSQAQ	-GI-S--T	--QS	-KPY--I	-I--IN	--L		287	
								d	e					
								****	*****					
HS1	181	HVSEI	SHDRV	KNPAD	VLTK	GDKVD	VKIL	ALDTE	KGRIS	LSIKAT	QRGP	WDEA	ADQIAAG	239
ES1	219	-ITD	MAWK--H	-SEIVNV--E	IT--V	-KF-R	-RT-V	-GL	-QLGED	-VAI	-KRYPE-		277	
RS1	225	--TDM	AWR--H	-SEIQNI-QQ	-K-Q	-IRINQ	-TH---GM	-QLESD---	GIGAKYPV-				283	
PS1	114	-ITD	MAWK--H	-SEIVNV--E	IT--V	-KF-R	-RT-V	-GL	-QLGED	-VAI	-KRYPE-		172	
CS1	288	---Q	-----SD	I-T--QP	--TLK-M	--SH	-R-R-V--T	-KLEPT-G-					337	
								a	b	c	d			
								****	*****	*****	****			

FIG. 3b

FIG. 3a

HS1	240	SVLEGT	KRVK	DFGAF	VEILP	GIEGL	VHVS	QISNK	RIENP	SEVLK	SGDKV	QVKVLD	KIP	298
ES1	278	TK-T	-R-	TNLT	-Y-	C----	EE-V-	-----	EM	RD-V-	DATL--	SV--	E-EA-	FTGVDR
RS1	284	KKIS	---	TNIT	-Y-	-----	LE-	-----	I-I-	EM	-RPG-QVI-	EFNK--	V-RAV--	-VDV
PS1	173	TK-T	-R-	TNLT	-Y-	C----	EE-V-	-----	EM				-K--	EIAAV--
														QVDA

e

HS1	299	AEERIS	LSMK	ALEE	KPERE	317
ES1	511	KNRA	---	VR-KD-	AD-KD	529
RS1	431	DK	---	GI-QL		442
PS1	320	ER	---	GV-QLA-	DP	335

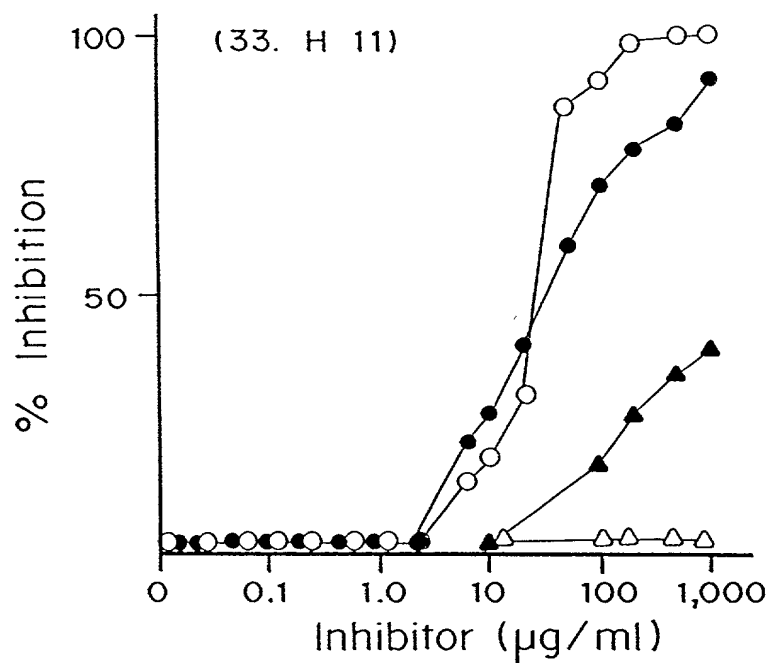


FIG. 4a

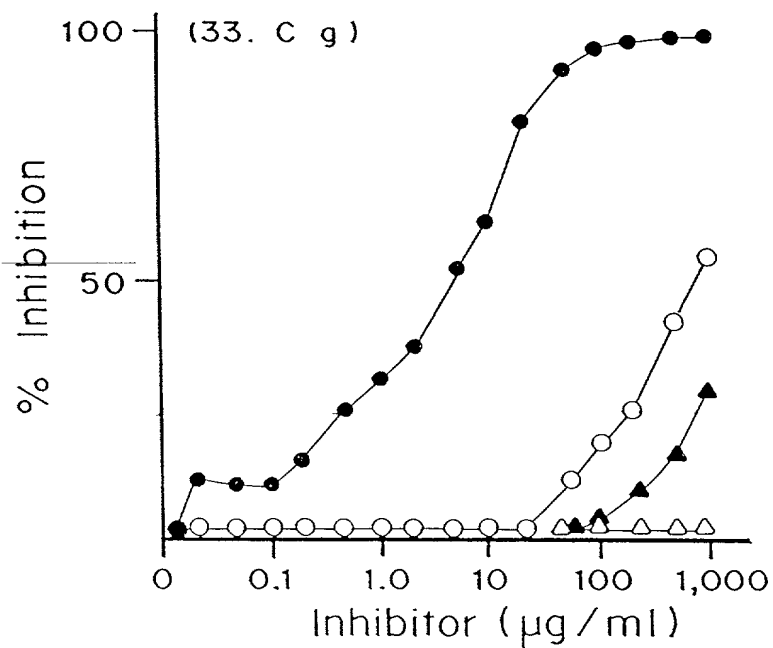


FIG. 4b

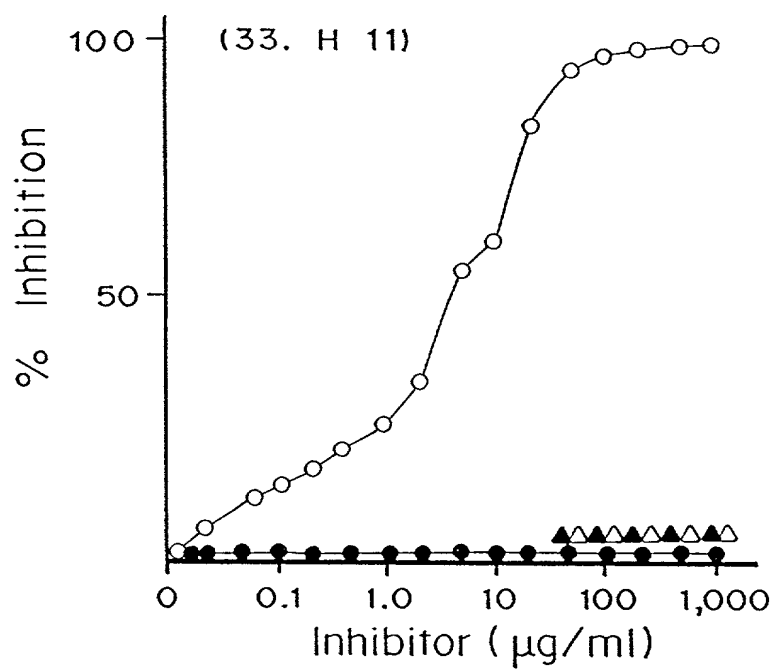


FIG. 4c

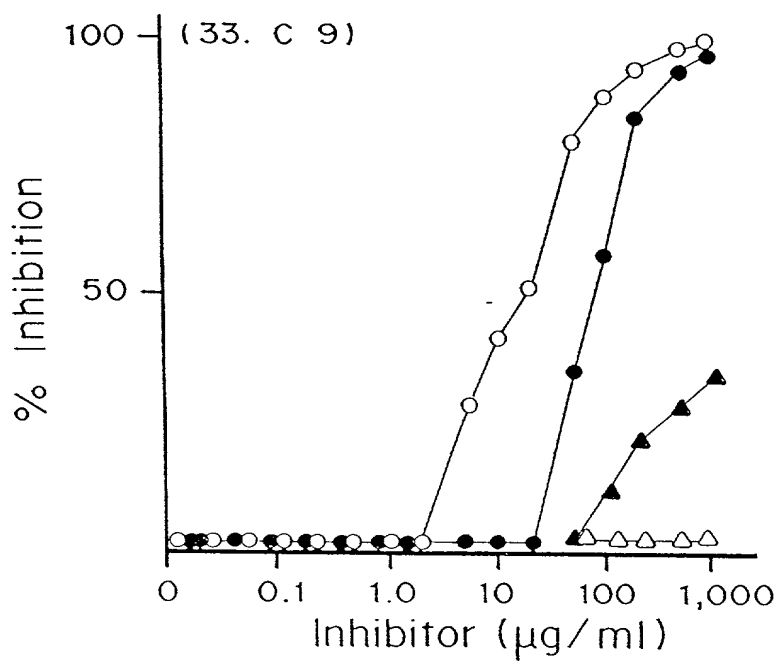


FIG. 4d